IN THE CLAIMS

Please cancel claims 17-19 and 22, amend claims 15 and 20-21, and add new claims 29-33.

1-14 (cancelled)

15. (currently amended) A method, comprising:

(a) selecting a Type II restriction endonuclease, the restriction endonuclease characterized by a modular structure having a specificity subunit and a catalytic subunit~~,~~ encoded by different genes; the specificity subunit further comprising at least one of an N-terminal domain for binding one half site of a bipartite recognition sequence, and a C-terminal domain for binding a second half site of the bipartite recognition sequence, and additionally a spacer;

(b) altering ~~modifying~~ the specificity subunit of the Type IIG restriction endonuclease by (i) changing the spacer region; (ii) tandemly duplicating the N-terminal or C-terminal domain; (iii) substituting part or all of the specificity subunit with a corresponding part or all of a specificity subunit from a second Type II restriction endonuclease, with a modular structure or from a DNA methylase with a modular structure; or (iv) mutating the specificity subunit of one or more of the domains; and

(c) obtaining the Type II restriction endonuclease with altered recognition sequence specificity.

16-19 (cancelled)

20. (currently amended) A method according to claim 15, ~~16, 17, 18 or 19,~~ wherein the specificity subunit has an N-terminal and a C-terminal

domain separated by the spacer region, ~~modifying the specificity subunit~~ wherein changing the spacer region further comprises changing a length of a spacer amino acid sequence between the N-terminal and C-terminal domains of the specificity ~~module~~ subunit.

21. (currently amended) A method according to claim 15 ~~18~~, wherein the second Type II restriction endonuclease or methyltransferase is selected from a group consisting of ~~a Type I restriction endonuclease,~~ a Type IIG restriction endonuclease and a γ-type m^6A methyltransferase.

22. (cancelled)

23. (withdrawn) A substantially pure Type IIG restriction endonuclease obtainable from *Citrobacter* species 2144 (NEB#1398) (ATCC Patent Accession No. PTA-5846) or from *Escherichia coli* NEB#1554 (ATCC Patent Accession No. PTA-5887) capable of recognizing at least one sequence selected from the group consisting of SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34 and SEQ ID NO:35, and cleaving the DNA on both sides of the recognition sequence.

24. (withdrawn) An isolated DNA encoding CstMI restriction endonuclease obtainable from *Escherichia coli* NEB#1554 (ATCC Patent Accession No. PTA-5887) or from *Citrobacter* species 2144 (NEB#1398) (ATCC Patent Accession No. PTA-5846).

25. (withdrawn) Isolated DNA encoding the restriction endonuclease of claim 1, wherein the DNA comprises a first DNA segment encoding an endonuclease and methyl transferase catalytic function and a second DNA segment encoding a sequence specificity function of the restriction

endonuclease wherein the first and second DNA segments comprise one or more DNA molecules.

26. (withdrawn) A recombinant DNA vector, comprising: at least one of a first DNA segment coding for the restriction and modification domains of CspCI restriction endonuclease and a second segment coding for the specificity domain of the restriction endonuclease.

27. (withdrawn) A host cell transformed with a first DNA segment coding for the restriction and modification domains of CspCI restriction endonuclease and a second segment coding for the specificity domain of the restriction endonuclease wherein the first DNA segment and the second DNA segment are contained within one or more DNA vectors.

28. (withdrawn) A method for obtaining the endonuclease of claim 23, comprising cultivating a sample of *Citrobacter* species 2144 (NEB#1398) or a host cell according to claim 6 under conditions favoring the production of the endonuclease; and purifying the endonuclease therefrom.

29. (new) A method; comprising:

(a) selecting a Type IIG restriction endonuclease characterized by a modular structure having a specificity subunit with an N-terminal domain, and a C-terminal domain separated by a spacer region encoded by a first gene and a catalytic subunit with endonuclease and methylase activity encoded by a second gene;

(b) altering the specificity of the Type IIG restriction endonuclease by modifying at least one of the N-terminal domain, the C-terminal domain or the spacer region; and

(c) obtaining the Type IIG restriction endonuclease with altered specificity.

30. (new) A method according to claim 29, wherein step (b) further comprises: changing the length of the spacer region.

31. (new) A method according to claim 29, wherein step (b) further comprises: tandemly duplicating the N-terminal or the C-terminal domain.

32. (new) A method according to claim 29, wherein step (b) further comprises: substituting part or all of its specificity subunit with a corresponding part or all of a specificity subunit from a second Type II restriction endonuclease with a modular structure or from a DNA methyltransferase with a modular structure;

33. (new) A method according to claim 29, wherein step (b) further comprises: mutating one or more of the N-terminal and C-terminal domains.